

Claims

- [c1] A bioinformatically detectable isolated oligonucleotide which is endogenously processed from a hairpin-shaped precursor, and anneals to a portion of a mRNA transcript of a target gene, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene, and wherein said oligonucleotide has at least 80% sequence identity with a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1–1436.
- [c2] A bioinformatically detectable isolated oligonucleotide which is endogenously processed from a hairpin-shaped precursor, and anneals to a portion of a mRNA transcript of a target gene selected from the group consisting of genes shown in Table 11, Row 1, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene, and wherein said oligonucleotide has at least 80% sequence identity with a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1–1436.
- [c3] A bioinformatically detectable isolated oligonucleotide having a nucleotide sequence selected from the group

consisting of SEQ ID NOs: 1–1436.

[c4] A bioinformatically detectable first oligonucleotide which is a portion of a mRNA transcript of a target gene, and anneals to a second oligonucleotide that is endogenously processed from a hairpin precursor, wherein binding of said first oligonucleotide to said second oligonucleotide represses expression of said target gene, and wherein nucleotide sequence of said second nucleotide is selected from the group consisting of SEQ ID NOs: 1–1436.

[c5] A bioinformatically detectable first oligonucleotide which is a portion of a mRNA transcript of a target gene selected from the group consisting of genes shown in Table 11 row 1, and anneals to a second oligonucleotide that is endogenously processed from a hairpin precursor, wherein binding of said first oligonucleotide to said second oligonucleotide represses expression of said target gene, and wherein nucleotide sequence of said second nucleotide is selected from the group consisting of SEQ ID NOs: 1–1436.

[c6] A bioinformatically detectable oligonucleotide having a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1–1436.

[c7] A bioinformatically detectable isolated oligonucleotide

which is endogenously processed from a hairpin-shaped precursor, and anneals to a portion of a mRNA transcript of a target gene associated with Multiple Sclerosis, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene.

[c8] A bioinformatically detectable isolated oligonucleotide which is endogenously processed from a hairpin-shaped precursor, and anneals to a portion of a mRNA transcript of a target gene that is differentially expressed in a tissue affected by Multiple Sclerosis relative an unaffected tissue, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene.

[c9] A bioinformatically detectable isolated oligonucleotide which is endogenously processed from a hairpin-shaped precursor, and anneals to a portion of a mRNA transcript of a target gene, the expression of which target gene correlates with Multiple Sclerosis or susceptibility thereto, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene.

[c10] A bioinformatically detectable isolated oligonucleotide which is endogenously processed from a hairpin-shaped precursor, and anneals to a portion of a mRNA transcript

of a target gene responsible for the formation of Multiple Sclerosis, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene.

[c11] A bioinformatically detectable isolated oligonucleotide which anneals to a portion of a mRNA transcript of a target gene selected from the group consisting of: CBLB, CNP, CTLA4, HLA-DRA, ICOS, IL12B, IL1RN, ITGA4, MCP, NCF1, NOTCH3, NRG1, PTPRC, PTPRZ1, SPP1 and TNFSF10, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene.

[c12] A bioinformatically detectable isolated oligonucleotide which is endogenously processed from a hairpin-shaped precursor, and anneals to a portion of a mRNA transcript of a target gene selected from the group consisting of: CBLB, CNP, CTLA4, HLA-DRA, ICOS, IL12B, IL1RN, ITGA4, MCP, NCF1, NOTCH3, NRG1, PTPRC, PTPRZ1, SPP1 and TNFSF10, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene.

[c13] A bioinformatically detectable isolated oligonucleotide which anneals to a portion of a mRNA transcript of a target gene selected from the group consisting of: CBLB,

CNP, CTLA4, HLA-DRA, ICOS, IL12B, IL1RN, ITGA4, MCP, NCF1, NOTCH3, NRG1, PTPRC, PTPRZ1, SPP1 and TNFSF10, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene, and wherein said oligonucleotide has at least 80% sequence identity with a nucleotide sequence selected from the group consisting of: (a) a sequence selected from the group consisting of SEQ ID NOs: 1, 4, 5, 8, 9, 14, 15, 17, 20, 22, 23, 24, 26, 27, 28, 29, 30, 31, 32, 35 and 4239-4700; and (b) the complement of a sequence selected from the group consisting of SEQ ID NOs: 7889, 7893, 7901, 7918, 7921, 7925, 7946, 8042, 8083, 8089, 8113, 8209, 8258, 8262, 8289, 8304, 8311, 8324, 8377 and 7887-8381.

[c14] A bioinformatically detectable oligonucleotide having a nucleotide sequence which has at least 80% sequence identity with a nucleotide sequence selected from the group consisting of: (a) a sequence selected from the group consisting of SEQ ID NOs: 1, 4, 5, 8, 9, 14, 15, 17, 20, 22, 23, 24, 26, 27, 28, 29, 30, 31, 32, 35 and 4239-4700; and (b) the complement of a sequence selected from the group consisting of SEQ ID NOs: 7889, 7893, 7901, 7918, 7921, 7925, 7946, 8042, 8083, 8089, 8113, 8209, 8258, 8262, 8289, 8304, 8311, 8324, 8377 and 7887-8381.

[c15] A bioinformatically detectable isolated oligonucleotide which anneals to a portion of a mRNA transcript of a target gene associated with Multiple Sclerosis, which target gene is selected from the group consisting of genes shown in Table 11, row 4, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene, and wherein said oligonucleotide has at least 80% sequence identity with a nucleotide sequence selected from the group consisting of: (a) a sequence selected from the group consisting of SEQ ID NOs: 1, 4, 5, 8, 9, 14, 15, 17, 20, 22, 23, 24, 26, 27, 28, 29, 30, 31, 32, 35 and 4239–4700; and (b) the complement of a sequence selected from the group consisting of SEQ ID NOs: 7889, 7893, 7901, 7918, 7921, 7925, 7946, 8042, 8083, 8089, 8113, 8209, 8258, 8262, 8289, 8304, 8311, 8324, 8377 and 7887–8381.

[c16] A bioinformatically detectable isolated oligonucleotide which anneals to a portion of a mRNA transcript of a target gene selected from the group consisting of: CBLB, CNP, CTLA4, HLA-DRA, ICOS, IL12B, IL1RN, ITGA4, MCP, NCF1, NOTCH3, NRG1, PTPRC, PTPRZ1, SPP1 and TNFSF10, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene, and wherein said oligonucleotide has at least 80% sequence identity with a nucleotide sequence selected

from the group consisting of SEQ ID NOs: 1, 4, 5, 8, 9, 14, 15, 17, 20, 22, 23, 24, 26, 27, 28, 29, 30, 31, 32 ,35 and 4239–4700.

[c17] A bioinformatically detectable isolated oligonucleotide which comprises from about 19 to about 22 nucleotides, which nucleotides are partially complementary to a target gene selected from the group consisting of: CBLB, CNP, CTLA4, HLA-DRA, ICOS, IL12B, IL1RN, ITGA4, MCP, NCF1, NOTCH3, NRG1, PTPRC, PTPRZ1, SPP1 and TNFSF10; and wherein said oligonucleotide is endogenously processed from a hairpin-form precursor, and comprises at least 19 contiguous nucleotides from a sequence selected from the group consisting of SEQ ID NOs: 1, 4, 5, 8, 9, 14, 15, 17, 20, 22, 23, 24, 26, 27, 28, 29, 30, 31, 32 ,35 and 4239cc4700.

[c18] A bioinformatically detectable first oligonucleotide which is a portion of a mRNA transcript of a target gene selected from the group consisting of genes shown in Table 11 row 4, and anneals to a second oligonucleotide that is endogenously processed from a hairpin precursor, wherein binding of said first oligonucleotide to said second oligonucleotide represses expression of said target gene.

[c19] A bioinformatically detectable first oligonucleotide which

is a portion of a mRNA transcript of a target gene selected from the group consisting of genes shown in Table 11 row 4, and anneals to a second oligonucleotide that is endogenously processed from a hairpin precursor, wherein binding of said first oligonucleotide to said second oligonucleotide represses expression of said target gene, and wherein nucleotide sequence of said second nucleotide is selected from the group consisting of SEQ ID NOs: 1, 4, 5, 8, 9, 14, 15, 17, 20, 22, 23, 24, 26, 27, 28, 29, 30, 31, 32 ,35 and 4239–4700.

[c20] A bioinformatically detectable isolated oligonucleotide which is endogenously processed from a hairpin-shaped precursor, and anneals to a portion of a mRNA transcript of a target gene associated with Alzheimers disease, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene.

[c21] A bioinformatically detectable isolated oligonucleotide which is endogenously processed from a hairpin-shaped precursor, and anneals to a portion of a mRNA transcript of a target gene that is differentially expressed in a tissue affected by Alzheimers disease relative an unaffected tissue, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene.

[c22] A bioinformatically detectable isolated oligonucleotide which is endogenously processed from a hairpin-shaped precursor, and anneals to a portion of a mRNA transcript of a target gene, the expression of which target gene correlates with Alzheimers disease or susceptibility thereto, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene.

[c23] A bioinformatically detectable isolated oligonucleotide which is endogenously processed from a hairpin-shaped precursor, and anneals to a portion of a mRNA transcript of a target gene responsible for the formation of Alzheimers disease, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene.

[c24] A bioinformatically detectable isolated oligonucleotide which anneals to a portion of a mRNA transcript of a target gene selected from the group consisting of genes shown in Table 11, row 2, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene.

[c25] A bioinformatically detectable isolated oligonucleotide which is endogenously processed from a hairpin-shaped precursor, and anneals to a portion of a mRNA transcript

of a target gene selected from the group consisting of genes shown in Table 11, row 2, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene.

[c26] A bioinformatically detectable isolated oligonucleotide which anneals to a portion of a mRNA transcript of a target gene associated with Alzheimers disease, which target gene is selected from the group consisting of genes shown in Table 11, row 2, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene, and wherein said oligonucleotide has at least 80% sequence identity with a nucleotide sequence selected from the group consisting of: (a) a sequence selected from the group consisting of SEQ ID NOs: 1-36 and 1437-4027; and (b) the complement of a sequence selected from the group consisting of SEQ ID NOs: 4999, 5017, 5084, 5137, 5246, 5293, 5319, 5455, 5489, 5538, 5587, 5637, 6039, 6050, 6274, 6334, 6347, 6362, 6417, 6433, 6478, 6575, 6606, 6685, 6809, 6827, 6843, 6869, 6892, 7045, 7321, 7353, 7383, 7442, 7445, 7468 and 4738-7634.

[c27] A bioinformatically detectable isolated oligonucleotide which anneals to a portion of a mRNA transcript of a target gene selected from the group consisting of genes shown in Table 11, row 2, wherein binding of said

oligonucleotide to said mRNA transcript represses expression of said target gene, and wherein said oligonucleotide has at least 80% sequence identity with a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1–36 and 1437–4027.

- [c28] A bioinformatically detectable isolated oligonucleotide which comprises from about 19 to about 22 nucleotides, which nucleotides are partially complementary to a target gene selected from the group consisting of genes shown in Table 11, row 2; and wherein said oligonucleotide is endogenously processed from a hairpin-form precursor, and comprises at least 19 contiguous nucleotides from a sequence selected from the group consisting of SEQ ID NOs: 1–36 and 1437–4027.
- [c29] A bioinformatically detectable first oligonucleotide which is a portion of a mRNA transcript of a target gene selected from the group consisting of genes shown in Table 11 row 2, and anneals to a second oligonucleotide that is endogenously processed from a hairpin precursor, wherein binding of said first oligonucleotide to said second oligonucleotide represses expression of said target gene.
- [c30] A bioinformatically detectable first oligonucleotide which is a portion of a mRNA transcript of a target gene se–

lected from the group consisting of genes shown in Table 11 row 2, and anneals to a second oligonucleotide that is endogenously processed from a hairpin precursor, wherein binding of said first oligonucleotide to said second oligonucleotide represses expression of said target gene, and wherein nucleotide sequence of said second nucleotide is selected from the group consisting of SEQ ID NOs: 1–36 and 1437–4027.

- [c31] A bioinformatically detectable isolated oligonucleotide which is endogenously processed from a hairpin-shaped precursor, and anneals to a portion of a mRNA transcript of a target gene associated with Duchenne disease, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene.
- [c32] A bioinformatically detectable isolated oligonucleotide which is endogenously processed from a hairpin-shaped precursor, and anneals to a portion of a mRNA transcript of a target gene that is differentially expressed in a tissue affected by Duchenne disease relative an unaffected tissue, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene.
- [c33] A bioinformatically detectable isolated oligonucleotide which is endogenously processed from a hairpin-shaped

precursor, and anneals to a portion of a mRNA transcript of a target gene, the expression of which target gene correlates with Duchenne disease or susceptibility thereto, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene.

[c34] A bioinformatically detectable isolated oligonucleotide which is endogenously processed from a hairpin-shaped precursor, and anneals to a portion of a mRNA transcript of a target gene responsible for the formation of Duchenne disease, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene.

[c35] A bioinformatically detectable isolated oligonucleotide which anneals to a portion of a mRNA transcript of a target gene selected from the group consisting of: CASQ1, DMD, ITGA7, LAMA2, NOS1 and SPARC, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene.

[c36] A bioinformatically detectable isolated oligonucleotide which is endogenously processed from a hairpin-shaped precursor, and anneals to a portion of a mRNA transcript of a target gene selected from the group consisting of: CASQ1, DMD, ITGA7, LAMA2, NOS1 and SPARC, wherein

binding of said oligonucleotide to said mRNA transcript represses expression of said target gene.

[c37] A bioinformatically detectable isolated oligonucleotide which anneals to a portion of a mRNA transcript of a target gene selected from the group consisting of: CASQ1, DMD, ITGA7, LAMA2, NOS1 and SPARC, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene, and wherein said oligonucleotide has at least 80% sequence identity with a nucleotide sequence selected from the group consisting of: (a) a sequence selected from the group consisting of SEQ ID NOs: 5, 8, 11, 14, 18, 24, 26, 27, 28, 29, 30, 33, 35, 36 and 4028–4238; and (b) the complement of a sequence selected from the group consisting of SEQ ID NOs: 7644, 7672, 7697, 7737, 7739, 7755, 7766, 7768, 7780, 7791, 7793, 7809, 7815, 7868 and 7635–7886.

[c38] A bioinformatically detectable isolated oligonucleotide which anneals to a portion of a mRNA transcript of a target gene associated with Duchenne disease, which target gene is selected from the group consisting of genes shown in Table 11, row 3, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene, and wherein said oligonucleotide has at least 80% sequence identity with a nucleotide sequence selected from the group consisting of:

(a) a sequence selected from the group consisting of SEQ ID NOs: 5, 8, 11, 14, 18, 24, 26, 27, 28, 29, 30, 33, 35, 36 and 4028–4238; and (b) the complement of a sequence selected from the group consisting of SEQ ID NOs: 7644, 7672, 7697, 7737, 7739, 7755, 7766, 7768, 7780, 7791, 7793, 7809, 7815, 7868 and 7635–7886.

[c39] A bioinformatically detectable isolated oligonucleotide which anneals to a portion of a mRNA transcript of a target gene selected from the group consisting of: CASQ1, DMD, ITGA7, LAMA2, NOS1 and SPARC, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene, and wherein said oligonucleotide has at least 80% sequence identity with a nucleotide sequence selected from the group consisting of SEQ ID NOs: 5, 8, 11, 14, 18, 24, 26, 27, 28, 29, 30, 33, 35, 36 and 4028–4238.

[c40] A bioinformatically detectable isolated oligonucleotide which comprises from about 19 to about 22 nucleotides, which nucleotides are partially complementary to a target gene selected from the group consisting of: CASQ1, DMD, ITGA7, LAMA2, NOS1 and SPARC; and wherein said oligonucleotide is endogenously processed from a hairpin-form precursor, and comprises at least 19 contiguous nucleotides from a sequence selected from the group consisting of SEQ ID NOs: 5, 8, 11, 14, 18, 24, 26,

27, 28, 29, 30, 33, 35, 36 and 4028–4238.

[c41] A bioinformatically detectable first oligonucleotide which is a portion of a mRNA transcript of a target gene selected from the group consisting of genes shown in Table 11 row 3, and anneals to a second oligonucleotide that is endogenously processed from a hairpin precursor, wherein binding of said first oligonucleotide to said second oligonucleotide represses expression of said target gene.

[c42] A bioinformatically detectable first oligonucleotide which is a portion of a mRNA transcript of a target gene selected from the group consisting of genes shown in Table 11 row 3, and anneals to a second oligonucleotide that is endogenously processed from a hairpin precursor, wherein binding of said first oligonucleotide to said second oligonucleotide represses expression of said target gene, and wherein nucleotide sequence of said second nucleotide is selected from the group consisting of SEQ ID NOs: 5, 8, 11, 14, 18, 24, 26, 27, 28, 29, 30, 33, 35, 36 and 4028–4238.

[c43] A bioinformatically detectable isolated oligonucleotide which anneals to a portion of a mRNA transcript of HEXA gene, wherein binding of said oligonucleotide to said mRNA transcript represses expression of HEXA gene.

[c44] A bioinformatically detectable isolated oligonucleotide which is endogenously processed from a hairpin-shaped precursor, and anneals to a portion of a mRNA transcript of HEXA gene, wherein binding of said oligonucleotide to said mRNA transcript represses expression of HEXA gene.

[c45] A bioinformatically detectable isolated oligonucleotide which anneals to a portion of a mRNA transcript of HEXA gene, wherein binding of said oligonucleotide to said mRNA transcript represses expression of HEXA gene, and wherein said oligonucleotide has at least 80% sequence identity with a nucleotide sequence selected from the group consisting of: (a) a sequence selected from the group consisting of SEQ ID NOs: 4,8,23 and 4701–4737; and (b) the complement of a sequence selected from the group consisting of SEQ ID NOs: 8400, 8401 and 8382–8405.

[c46] A bioinformatically detectable oligonucleotide having a nucleotide sequence which has at least 80% sequence identity with a nucleotide sequence selected from the group consisting of: (a) a sequence selected from the group consisting of SEQ ID NOs: 4,8,23 and 4701–4737; and (b) the complement of a sequence selected from the group consisting of SEQ ID NOs: 8400, 8401 and

8382–8405.

- [c47] A bioinformatically detectable isolated oligonucleotide which anneals to a portion of a mRNA transcript of HEXA gene, wherein binding of said oligonucleotide to said mRNA transcript represses expression of HEXA gene, and wherein said oligonucleotide has at least 80% sequence identity with a nucleotide sequence selected from the group consisting of SEQ ID NOs: 4,8,23 and 4701–4737.
- [c48] A bioinformatically detectable isolated oligonucleotide which is endogenously processed from a hairpin-shaped precursor, and anneals to a complementary portion of a mRNA transcript of HEXA gene, wherein binding of said oligonucleotide to said mRNA transcript represses expression of HEXA gene, and wherein said oligonucleotide has at least 80% sequence identity with a nucleotide sequence selected from the group consisting of SEQ ID NOs: 4,8,23 and 4701–4737, and.
- [c49] A bioinformatically detectable isolated oligonucleotide which comprises from about 19 to about 22 nucleotides, which nucleotides anneal to a portion of a mRNA transcript of HEXA gene; and wherein said oligonucleotide is endogenously processed from a hairpin-form precursor, and comprises at least 19 contiguous nucleotides from a sequence selected from the group consisting of SEQ ID

NOs: 4,8,23 and 4701–4737.

- [c50] A bioinformatically detectable first oligonucleotide which is a portion of a mRNA transcript of HEXA gene, and anneals to a second oligonucleotide that is endogenously processed from a hairpin precursor, wherein binding of said first oligonucleotide to said second oligonucleotide represses expression of said target gene.
- [c51] A bioinformatically detectable first oligonucleotide which is a portion of a mRNA transcript of HEXA gene, and anneals to a second oligonucleotide that is endogenously processed from a hairpin precursor, wherein binding of said first oligonucleotide to said second oligonucleotide represses expression of said target gene, and wherein nucleotide sequence of said second nucleotide is selected from the group consisting of SEQ ID NOs: 4,8,23 and 4701–4737.
- [c52] A bioinformatically detectable isolated oligonucleotide which anneals to a portion of a mRNA transcript of APP gene, wherein binding of said oligonucleotide to said mRNA transcript represses expression of APP gene.
- [c53] A bioinformatically detectable isolated oligonucleotide which is endogenously processed from a hairpin-shaped precursor, and anneals to a portion of a mRNA transcript

of APP gene, wherein binding of said oligonucleotide to said mRNA transcript represses expression of APP gene.

[c54] A bioinformatically detectable isolated oligonucleotide which anneals to a portion of a mRNA transcript of APP gene, wherein binding of said oligonucleotide to said mRNA transcript represses expression of APP gene, and wherein said oligonucleotide has at least 80% sequence identity with a nucleotide sequence selected from the group consisting of: (a) a sequence selected from the group consisting of SEQ ID NOs: 2, 34 and 1757–1768; and (b) the complement of a sequence selected from the group consisting of SEQ ID NOs: 5097, 5104, 32101, 120890 and 5097–5112.

[c55] A bioinformatically detectable isolated oligonucleotide which anneals to a portion of a mRNA transcript of APP gene, wherein binding of said oligonucleotide to said mRNA transcript represses expression of APP gene, and wherein said oligonucleotide has at least 80% sequence identity with a nucleotide sequence selected from the group consisting of SEQ ID NOs: 2, 34 and 1757–1768.

[c56] A bioinformatically detectable isolated oligonucleotide which is endogenously processed from a hairpin-shaped precursor, and anneals to a complementary portion of a mRNA transcript of APP gene, wherein binding of said

oligonucleotide to said mRNA transcript represses expression of APP gene, and wherein said oligonucleotide has at least 80% sequence identity with a nucleotide sequence selected from the group consisting of SEQ ID NOs: 2, 34 and 1757–1768.

[c57] A bioinformatically detectable isolated oligonucleotide which comprises from about 19 to about 22 nucleotides, which nucleotides anneal to a portion of a mRNA transcript of APP gene; and wherein said oligonucleotide is endogenously processed from a hairpin-form precursor, and comprises at least 19 contiguous nucleotides from a sequence selected from the group consisting of SEQ ID NOs: 2, 34 and 1757–1768.

[c58] A bioinformatically detectable first oligonucleotide which is a portion of a mRNA transcript of APP gene, and anneals to a second oligonucleotide that is endogenously processed from a hairpin precursor, wherein binding of said first oligonucleotide to said second oligonucleotide represses expression of said target gene.

[c59] A bioinformatically detectable first oligonucleotide which is a portion of a mRNA transcript of APP gene, and anneals to a second oligonucleotide that is endogenously processed from a hairpin precursor, wherein binding of said first oligonucleotide to said second oligonucleotide

represses expression of said target gene, and wherein nucleotide sequence of said second nucleotide is selected from the group consisting of SEQ ID NOs: 2, 34 and 1757–1768.

[c60] A bioinformatically detectable isolated polynucleotide which is endogenously processed into a plurality of hairpin shaped precursor oligonucleotides, each of which is endogenously processed into a respective oligonucleotide, which in turn anneals to a portion of a mRNA transcript of a target gene, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene.

[c61] A bioinformatically detectable isolated oligonucleotide which is endogenously processed from a hairpin-shaped precursor, and anneals to a portion of a mRNA transcript of a target gene, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene, and wherein said target gene does not encode a protein.

[c62] A bioinformatically detectable isolated oligonucleotide which is endogenously processed from a hairpin-shaped precursor, and anneals to a portion of a mRNA transcript of a target gene, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said

target gene, and wherein a function of said oligonucleotide comprises modulation of cell type.

[c63] A bioinformatically detectable isolated oligonucleotide which is endogenously processed from a hairpin-shaped precursor, and anneals to a portion of a mRNA transcript of a target gene, wherein binding of said oligonucleotide to said mRNA transcript represses expression of said target gene, and wherein said oligonucleotide is maternally transferred by a cell to at least one daughter cell of said cell, and a function of said oligonucleotide comprises modulation of cell type of said daughter cell.

[c64] A method for bioinformatic detection of microRNA oligonucleotides, the method comprising: bioinformatically detecting a hairpin shaped precursor oligonucleotide; bioinformatically detecting an oligonucleotide which is endogenously processed from said hairpin shaped precursor oligonucleotide; and bioinformatically detecting a target gene of said oligonucleotide wherein said oligonucleotide anneals to at least one portion of a mRNA transcript of said target gene, and wherein said binding represses expression of said target gene, and said target gene is associated with a disease.